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## SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: Philip E.Branton et al.

(ii) TITLE OF THE INVENTION: Adenovirus E4 Protein For  
Inducing Cell Death

(iii) NUMBER OF SEQUENCES: 4

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Clark &amp; Elbing LLP

(B) STREET: 176 Federal Street

(C) CITY: Boston

(D) STATE: MA

(E) COUNTRY: USA

(F) ZIP: 02110

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 3 July 1997

(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/021,273

(B) FILING DATE: 5 July 1996

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/028,740

(B) FILING DATE: 22 October 1996

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bieker-Brady, Kristina

(B) REGISTRATION NUMBER: 39,109

(C) REFERENCE/DOCKET NUMBER: 50013/002WO1

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-428-0200

(B) TELEFAX: 617-428-7045

(C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 885 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10 ATGACTACGT CCGGCGTTCC ATTTGGCATG AACTACGAC CAACACGATC TCGGTTGTCT 60  
 CCGGCGCACTC CGTACAGTAG GGATCGTCTA CCTCCTTTTG AGACAGAAAC CCGCGCTACC 120  
 ATACTGGAGG ATCATCCGCT GCTGCCCGAA TGTAACTT TGACAATGCA CAACGTGAGT 180  
 TACGTGCGAG GTCTTCCCTG CAGTGTGGGA TTTACGCTGA TTCAGGAATG GGTGTGTTCCC 240  
 TGGGATATGG TTCTAACGCG GGAGGAGCTT GTAATCCTGA GGAAGTGTAT GCACGTGTGC 300  
 CTGTGTTGTG CCAACATTGA TATCATGACG AGCATGATGA TCCATGGTTA CGAGTCCTGG 360  
 GCTCTCCACT GTCATTGTTC CAGTCCCGGT TCCCTGCAGT GTATAGCCGG CGGGCAGGTT 420  
 TTGGCCAGCT GGTTAGGAT GGTGGTGGAT GCGGCCATGT TTAATCAGAG GTTTATATGG 480  
 15 TACCGGGAGG TGGTGAATTA CAACATGCCA AAAGAGGTAA TGTATTATGTC CAGCGTGTTT 540  
 ATGAGGGGTC GCCACTTAAT CTACCTGCGC TTGTGGTATG ATGGCCACGT GGGTTCTGTG 600  
 GTCCCCGCCA TGAGCTTTGG ATACAGCGCC TTGCACTGTG GGATTTTGAA CAATATTGTG 660  
 GTGCTGTGCT GCAGTTACTG TGCTGATTTA AGTGAGATCA GGGTGCCTG CTGTGCCCGG 720  
 AGGACAAGGC GCCTTATGCT GCGGGCGGTG CGAATCATCG CTGAGGAGAC CACTGCCATG 780  
 20 TTGTATTCTT GCAGGACGGA GCGGCGGCGG CAGCAGTTTA TTCGCGCGCT GCTGCAGCAC 840  
 CACCGCCCTA TCCTGATGCA CGATTATGAC TCTACCCCA TGTAG 885

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 294 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Thr Thr Ser Gly Val Pro Phe Gly Met Thr Leu Arg Pro Thr Arg  
 1 5 10 15  
 Ser Arg Leu Ser Arg Arg Thr Pro Tyr Ser Arg Asp Arg Leu Pro Pro  
 20 25 30  
 Phe Glu Thr Glu Thr Arg Ala Thr Ile Leu Glu Asp His Pro Leu Leu  
 35 40 45  
 Pro Glu Cys Asn Thr Leu Thr Met His Asn Val Ser Tyr Val Arg Gly  
 50 55 60  
 Leu Pro Cys Ser Val Gly Phe Thr Leu Ile Gln Glu Trp Val Val Pro  
 65 70 75 80  
 40 Trp Asp Met Val Leu Thr Arg Glu Glu Leu Val Ile Leu Arg Lys Cys  
 85 90 95  
 Met His Val Cys Leu Cys Cys Ala Asn Ile Asp Ile Met Thr Ser Met  
 100 105 110  
 Met Ile His Gly Tyr Glu Ser Trp Ala Leu His Cys His Cys Ser Ser  
 115 120 125  
 45 Pro Gly Ser Leu Gln Cys Ile Ala Gly Gly Gln Val Leu Ala Ser Trp  
 130 135 140

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5 Phe Arg Met Val Val Asp Gly Ala Met Phe Asn Gln Arg Phe Ile Trp  
 145 150 155 160  
 Tyr Arg Glu Val Val Asn Tyr Asn Met Pro Lys Glu Val Met Phe Met  
 165 170 175  
 10 Ser Ser Val Phe Met Arg Gly Arg His Leu Ile Tyr Leu Arg Leu Trp  
 180 185 190  
 Tyr Asp Gly His Val Gly Ser Val Val Pro Ala Met Ser Phe Gly Tyr  
 195 200 205  
 Ser Ala Leu His Cys Gly Ile Leu Asn Asn Ile Val Val Leu Cys Cys  
 210 215 220  
 15 Ser Tyr Cys Ala Asp Leu Ser Glu Ile Arg Val Arg Cys Cys Ala Arg  
 225 230 235 240  
 Arg Thr Arg Arg Leu Met Leu Arg Ala Val Arg Ile Ile Ala Glu Glu  
 245 250 255  
 20 Thr Thr Ala Met Leu Tyr Ser Cys Arg Thr Glu Arg Arg Arg Gln Gln  
 260 265 270  
 Phe Ile Arg Ala Leu Leu Gln His Arg Pro Ile Leu Met His Asp  
 275 280 285  
 Tyr Asp Ser Thr Pro Met  
 290

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGTTCTTC CAGCTCTTCC CGCTCCTCCC GTGTGTGACT CGCAGAACGA ATGTGTAGGT 60  
 TGGCTGGGTG TGGCTTATTC TGGCGTGGTG GATGTTATCA GGGCAGCGGC GCATGAAGGA 120  
 GTTTACATAG AACCCGAAGC CAGGGGGCGC CTGGATGCTT TGAGAGAGTG GATATACTAC 180  
 AACTACTACA CAGAGCGATC TAAGCGGCGA GACCGGAGAC GCAGATCTGT TTGTCACGCC 240  
 CGCACCTGGT TTTGCTTCAG GAAATATGAC TACGTCCGGC GTTCCATTG GCATGACACT 300  
 ACGACCAACA CGATCTCGGT TGTCTCGGCG CACTCCGTAC AGTAG 345

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Leu Pro Ala Leu Pro Ala Pro Pro Val Cys Asp Ser Gln Asn  
 1 5 10 15

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Glu Cys Val Gly Trp Leu Gly Val Ala Tyr Ser Ala Val Val Asp Val  
                   20                  25                  30  
 Ile Arg Ala Ala Ala His Glu Gly Val Tyr Ile Glu Pro Glu Ala Arg  
                   35                  40                  45  
 5 Gly Arg Leu Asp Ala Leu Arg Glu Trp Ile Tyr Tyr Asn Tyr Tyr Thr  
           50                  55                  60  
 Glu Arg Ser Lys Arg Arg Asp Arg Arg Arg Arg Ser Val Cys His Ala  
 65                  70                  75                  80  
 10 Arg Thr Trp Phe Cys Phe Arg Lys Tyr Asp Tyr Val Arg Arg Ser Ile  
                   85                  90                  95  
 Trp His Asp Thr Thr Thr Asn Thr Ile Ser Val Val Ser Ala His Ser  
                   100                  105                  110  
 Val Gln

What is claimed is:

1. A polypeptide having the amino acid sequence: